```
  1 GAATTCCGGCGCGGAGGCCGAGAGAGAAGTCACTTGCCCTGGCTCTACCTTGAAGTGGTTCTCAGGGTTGGGGCGAGAGTCGGGGTGGGGACCGAGATGC

101 AGCTCTATCCTGTGCCCCTGGTCGCAGCAGGCAGCCCAGCGCTTCGCGTGTTCTACTTGGCCTGTCCGCTGCCGCCTAATGAGCTCAGGTCTAGGCCGAG

201 CAGAGGGGGCACCTGGTCGGACTCGGTTGGGCTCGGGCGGCCCCGCCTCCCCCCGCCCGCCAGGCGGGCCCTTCTCGACGGCGCGGGGCGGGCCCTGCGG

301 GCGCGGGGCTGAAGGCGGAACCACGACGGGCAGAGAGCACGGAGCCGGGAAGCCCCTGGGCGCCCGTCGGAGGGCTATGGAGCAGCGGCCGCGGGGCTGC
  1                                                                                   M  E  Q  R  P  R  G  C

401 GCGGCGGTGGCGGCGGCGCTCCTCCTGGTGCTGCTGGGGGCCCGGGCCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGA
  9 A  A  V  A  A  A  L  L  L  V  L  L  G  A  R  A  Q  G  G  T  R  S  P  R  C  D  C  A  G  D  F  H  K  K

501 AGATTGGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCTTGCACGGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGTCCCCA
 43   I  G  L  F  C  C  R  G  C  P  A  G  H  Y  L  K  A  P  C  T  E  P  C  G  N  S  T  C  L  V  C  P  Q

601 AGACACCTTCTTGGCCTGGGAGAACCACCATAATTCTGAATGTGCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGCGCTGGAGAACTGTTCA
 76  D  T  F  L  A  W  E  N  H  H  N  S  E  C  A  R  C  Q  A  C  D  E  Q  A  S  Q  V  A  L  E  N  C  S

701 GCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGTGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTGCCAACCATGCC
109 A  V  A  D  T  R  C  G  C  K  P  G  W  F  V  E  C  Q  V  S  Q  C  V  S  S  S  P  F  Y  C  Q  P  C  L

801 TAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGCGATGG
143   D  C  G  A  L  H  R  H  T  R  L  L  C  S  R  R  D  T  D  C  G  T  C  L  P  G  F  Y  E  H  G  D  G

901 CTGCGTGTCCTGCCCCACGTAATTCCTAGCTGTCGTGGGATGGAGGGAAGGGCGGCTGGGAGCAGAGCAGGGGCCTGGGGTGGGGCAGGTGCTGCTGGTT
176  C  V  S  C  P  T

1001 CAGGAATAGGAAGAGGGGATAGGGAGGAGGGAGCCTTGGCCCTGTGATGGGTGGGCCCCACTTCAGGCAAACTTAGATGGCAAAAGAGCAATCTGGATCC

1101 GCCTTAGCCAGATACATAAGGGTATTTGCCTTCACTTTCAGCCAGCATTCCCCCCAGCGATCCTAGCCAGATATTACAGATGATTTGTCACTTACACAGA

1201 GAGTCACATTGATATAGCTTTAAAACTTGGGCTGAAGGAGGTTGAGGCTGCAGTGAGCTATGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCGAG

1301 ACCTATTAAATAAATAAATAAATATTAAATCTATTAAATATTAAATATTAAATCTATTAAATAAATAAATACAAAGGGCTGAGAGTCAGGACTGTGCTGC

1401 TAGTTCTCTAGGGGATCTTGGGCAAGTGCAGAGAATTC
```

FIG. 1


hApo2LI 34 D C A G D - - - - F H K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L - - - - - - - - -
hTNFR1 43 V C P Q G K - - Y I H P Q N N S I C C T K C H K G T Y L Y N D C P G P G Q D T D C R - - - - - - - - -
hTNFR2 39 T C R L R E - - - Y Y D Q T A Q M C C S K C S P G Q H A K V F C T K T - S D T V C D - - - - - - - - -
hTNFRrp 42 T C R D Q E K E - Y Y E P Q H R I C C S R C P P G T Y V S A K C S R I - R D T V C A - - - - - - - - -
hFAS/Apo1 48 N L E G L - - - - - - H H D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V - - - - - - - - -
hLNGFR 31 A C P T G - - - - - L Y T H S G E C C K A C N L G E G V A Q P C G A - - N Q T V C E - - - - - - - - -
hCD40 25 A C R E K - - - - - Q Y L I N S Q C C S L C Q P G Q K L V S D C T E F - T E T E C L - - - - - - - - -
hCD27 26 S C P E R - - - - H Y W A Q G K L C C Q M C E P G T F L V K D C D Q H R K A A Q C D - - - - - - - - -
hCD30 28 T C H G N P S H - Y Y D K A V R R C C Y R C P M G L F P T Q Q C P Q R - - P T D C R K - - - - - - - - -
hOX40 30 H C V G D T - - - - - Y P S N D R C C H E C R P G N G M V S R C S R S - Q N T V C R - - - - - - - - -
hApo2LI 72 V C P Q D - T F L A W E N H H S E C A R C - Q A C D E Q A S Q V A L E N C S A V A D T R C G - - - -
hTNFR1 83 E C E S G - S F T A S E N H L R H C L S C - S K C R K E M G Q V E I S S C T V D R D T V C G - - - -
hTNFR2 77 S C E D S T Y T Q L W N W V - P E C L S C G S R C S S - - D Q V E T Q A C T R E Q N R I C T - - - -
hTNFRrp 82 T C A E N S Y N E H W N Y L - T I C Q L C - R P C D P V M G L E E I A P C T S K R K T Q C R - - - -
hFAS/Apo1 84 P C Q E G K E Y T D K A H F S S K C R R C - R L C D E G H G L E V E I N C T R T Q N T K C R - - - -
hLNGFR 66 P C L D S V T F S D V V S A T E P C K P C - T E C V G L - - Q S M S A P C V E A D D A V C R - - - -
hCD40 61 P C G E S E F L D T W N R E - T H C H Q H - K Y C D P N L G L R V Q Q K G T S E T D T I C T - - - -
hCD27 64 P C I P G V S F S P D H H T R P H C E S C - R H C N S G L L V R - - - N C T I T A N A E C A - - - -
hCD30 68 Q C E P D - Y Y L D E A D R - - - C T A C - V T C S R D D L V E K T - P C A W N S S R V C E - - - -
hOX40 66 P C G P G - F Y N D V V S S K P - C K P C - T W C N L R S G S E R K Q L C T A T Q D T V C R - - - -

FIG. 2A

```
hApo2LI     116  C K P G W F V E C Q V S Q C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R R D - T D C G - T
hTNFR1      127  C R K N Q Y R H Y W S E N L - - - - - F Q C F N C S L C L N G - - T V H L S C Q E K Q N T V C - - T
hTNFR2      120  C R P G W Y C A L S K Q E G C - - - - R L C A P L R K C R P G - F G V A R P G T E T S D V V C K - P
hTNFRrp     126  C Q P G M F C A A W A L E C - - - - - T H C E L L S D C P P G T E A E L K D E V G K G N N H C V - P
hFAS/Apo1   129  C K P N F F - - C N S T V C - - - - - E H C D P C T K C E H G I - - - I K E C T L T S N T K C K -
hLNGFR      109  C A Y G Y Y Q D E T T - - - - - - - - G R C E A C R V C E A G S G L - V F S C Q D K Q N T V C E - E
hCD40       105  C E E G W H C T S E A C - - - - - - - E S C V L H R S C S P G F G - V K Q I A T G V S D T I C E - P
hCD27       106  C R N G W Q C R D K E C - - - - - - - T E C D P L P N P S L T A R S S Q A L S P H P Q P T H L P -
hCD30       108  - C R P G M F C S T S A V N S C - - - - A R C F F H S V C P A G M I V K F P G T A Q K - N T V C E -
hOX40       109  - C R A G T Q P L D S Y K P G - - - - - V D C A - - - - - - - - - - - - - - - - - - - - - - - - - -

hApo2LI     164  C L P G F Y E H G D - - - - G C V S C P T
hTNFR1      168  C H A G F F L R E N - - - - E C V S C S N C K K - - - - S L E C T K - - - - - L C L
hTNFR2      164  C A P G T F S N T T S S T D I C R P H Q I C N V V A I P G N A S M - - - - D A V C T
hTNFRrp     170  C K A G H F Q N T S S P S A R C Q P H T R C E N Q G L V E A A P G T A Q S D T T C K
hLNGFR      149  C P D G T Y S D E A N H V D P C L P C T V C E D T E R Q L R E C T R W - A D A E C E
hCD40       146  C P V G F F S N V S S A F E K C H P W T S C E T K D L V V Q Q A G T N K T D V V C G
hOX40       127  P C P P G H F S P G D - - N Q A C K P W T N C T L A G K H T L Q P A S N S S D A I C E
```

FIG. 2B

```
  1 CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GCCAGAGAGC ACGGAGCCGG

 61 GAAGCCCCTG GGCGCCCGTC GGAGGGCTAT GGAGCAGCGG CCGCGGGGCT GCGCGGCGGT
  1                                  M  E  Q  R  P  R  G  C  A  A  V

121 GGCGGCGGCG CTCCTCCTGG TGCTGCTGGG GGCCCGGGCC CAGGGCGGCA CTCGTAGCCC
 12  A  A  A  L  L  L  V  L  L  G  A  R  A  Q  G  G  T  R  S  P

181 CAGGTGTGAC TGTGCCGGTG ACTTCCACAA GAAGATTGGT CTGTTTTGTT GCAGAGGCTG
 32  R  C  D  C  A  G  D  F  H  K  K  I  G  L  F  C  C  R  G  C

241 CCCAGCGGGG CACTACCTGA AGGCCCCTTG CACGGAGCCC TGCGGCAACT CCACCTGCCT
 52  P  A  G  H  Y  L  K  A  P  C  T  E  P  C  G  N  S  T  C  L
                                                  *

301 TGTGTGTCCC CAAGACACCT TCTTGGCCTG GGAGAACCAC CATAATTCTG AATGTGCCCG
 72  V  C  P  Q  D  T  F  L  A  W  E  N  H  H  N  S  E  C  A  R

361 CTGCCAGGCC TGTGATGAGC AGGCCTCCCA GGTGGCGCTG GAGAACTGTT CAGCAGTGGC
 92  C  Q  A  C  D  E  Q  A  S  Q  V  A  L  E  N  C  S  A  V  A
                                              *

421 CGACACCCGC TGTGGCTGTA AGCCAGGCTG GTTTGTGGAG TGCCAGGTCA GCCAATGTGT
112  D  T  R  C  G  C  K  P  G  W  F  V  E  C  Q  V  S  Q  C  V

481 CAGCAGTTCA CCCTTCTACT GCCAACCATG CCTAGACTGC GGGGCCCTGC ACCGCCACAC
132  S  S  S  P  F  Y  C  Q  P  C  L  D  C  G  A  L  H  R  H  T
```

FIG. 4A

```
541 ACGGCTACTC TGTTCCCGCA GAGATACTGA CTGTGGGACC TGCCTGCCTG GCTTCTATGA
152  R  L  L   C  S  R  R   D  T  D   C  G  T   C  L  P  G   F  Y  E

601 ACATGGCGAT GGCTGCGTGT CCTGCCCCAC GAGCACCCTG GGGAGCTGTC CAGAGCGCTG
172  H  G  D   G  C  V  S   C  P  T   S  T  L   G  S  C  P   E  R  C

661 TGCCGCTGTC TGTGGCTGGA GGCAGATGTT CTGGGTCCAG GTGCTCCTGG CTGGCCTTGT
192  A  A  V   C  G  W  R   Q  M  F   W  V  Q   V  L  L  A   G  L  V

721 GGTCCCCCTC CTGCTTGGGG CCACCCTGAC CTACACATAC CGCCACTGCT GGCCTCACAA
212  V  P  L   L  L  G  A   T  L  T   Y  T  Y   R  H  C  W   P  H  K

781 GCCCCTGGTT ACTGCAGATG AAGCTGGGAT GGAGGCTCTG ACCCCACCAC CGGCCACCCA
232  P  L  V   T [A] D  E   A  G  M   E  A  L   T  P  P  P   A  T  H

841 TCTGTCACCC TTGGACAGCG CCCACACCCT TCTAGCACCT CCTGACAGCA GTGAGAAGAT
252  L  S  P   L  D  S  A   H  T  L   L  A  P   P  D  S  S   E  K  I

901 CTGCACCGTC CAGTTGGTGG GTAACAGCTG GACCCCTGGC TACCCCGAGA CCCAGGAGGC
272  C  T  V   Q  L  V  G   N  S  W   T  P  G   Y  P  E  T   Q  E  A

961 GCTCTGCCCG CAGGTGACAT GGTCCTGGGA CCAGTTGCCC AGCAGAGCTC TTGGCCCCGC
292  L  C  P   Q  V  T  W   S  W  D   Q  L  P   S  R  A  L   G  P  A

1021 TGCTGCGCCC ACACTCTCGC CAGAGTCCCC AGCCGGCTCG CCAGCCATGA TGCTGCAGCC
312  A  A  P   T  L  S  P   E  S  P   A  G  S   P  A  M  M   L  Q  P
```

FIG. 4B

```
1081 GGGCCCGCAG CTCTACGACG TGATGGACGC GGTCCCAGCG CGGCGCTGGA AGGAGTTCGT
 332  G  P  Q   L  Y  D  V  M  D  A  V  P  A  R  R  W  K  E  F  V

1141 GCGCACGCTG GGGCTGCGCG AGGCAGAGAT CGAAGCCGTG GAGGTGGAGA TCGGCCGCTT
 352  R  T  L   G  L  R  E  A  E  I  E  A  V  E  V  E  I  G  R  F

1201 CCGAGACCAG CAGTACGAGA TGCTCAAGCG CTGGCGCCAG CAGCAGCCCG CGGGCCTCGG
 372  R  D  Q   Q  Y  E  M  L  K  R  W  R  Q  Q  Q  P  A  G  L  G

1261 AGCCGTTTAC GCGGCCCTGG AGCGCATGGG GCTGGACGGC TGCGTGGAAG ACTTGCGCAG
 392  A  V  Y   A  A  L  E  R  M  G  L  D  G  C  V  E  D  L  R  S

1321 CCGCCTGCAG CGCGGCCCGT GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC
 412  R  L  Q   R  G  P

1381 TTGCAGAAGC CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC

1441 CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC CCCTATCGCT

1501 CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG GTGAAGACAT TTCTCAACTT

1561 CTCGGCCGGA GTTTGGCTGA GATCGCGGTA TTAAATCTGT GAAAGAAAAC AAAAAAAAAA

1621 AAAAAAAAAA AAAA
```

FIG. 4C

```
Apo3       1  MEQRPRGCAAVAAALLLVLLGARAQGGTRSPR------------
TNFR1      1  MGLSTVPDLLLPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV
Fas/Apo1   1  MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV

Apo3      33  CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLV
TNFR1     44  CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRE
Fas/Apo1  45  ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVP

Apo3      73  CPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG
TNFR1     85  CESGSFTASENHLRH-CLSCSKCRKEMGQVEISSCTVDRDTVCG
Fas/Apo1  85  CQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCR

Apo3     117  CKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRD-TDCGT
TNFR1    127  CRKNQYRHYWSENLFQ-----CFNCSLCLNGTVHLS--CQEKQNTVCT-
Fas/Apo1 129  CKPNFF--CNSTVCEH-----CDPCTKCEHGIIKE---CTLTSNTKCKE

Apo3     165  CLPGFYEHGDGCVSCPTSTLGSCP--ERCAAVCGW
TNFR1    168  CHAGFFLRENECVSCS-----NCKKSLECTKLCLP
```

FIG. 5

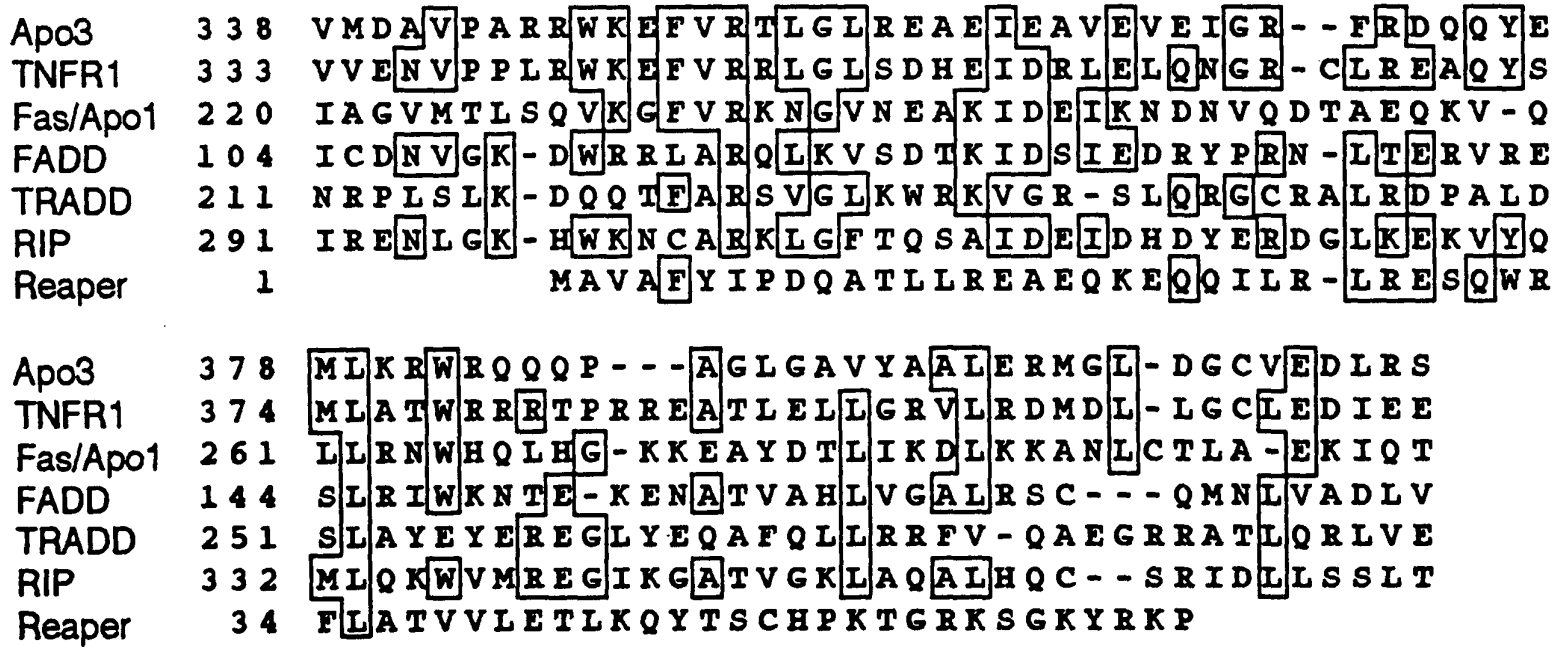
Apo3 338 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR--FRDQQYE
TNFR1 333 VVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR-CLREAQYS
Fas/Apo1 220 IAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKV-Q
FADD 104 ICDNVGK-DWRRLARQLKVSDTKIDSIEDRYPRN-LTERVRE
TRADD 211 NRPLSLK-DQQTFARSVGLKWRKVGR-SLQRGCRALRDPALD
RIP 291 IRENLGK-HWKNCARKLGFTQSAIDEIDHDYERDGLKEKVYQ
Reaper 1 MAVAFYIPDQATLLREAEQKEQQILR-LRESQWR
Apo3 378 MLKRWRQQQP---AGLGAVYAALERMGL-DGCVEDLRS
TNFR1 374 MLATWRRRTPRREATLELLGRVLRDMDL-LGCLEDIEE
Fas/Apo1 261 LLRNWHQLHG-KKEAYDTLIKDLKKANLCTLA-EKIQT
FADD 144 SLRIWKNTE-KENATVAHLVGALRSC---QMNLVADLV
TRADD 251 SLAYEYEREGLYEQAFQLLRRFV-QAEGRRATLQRLVE
RIP 332 MLQKWVMREGIKGATVGKLAQALHQC--SRIDLLSSLT
Reaper 34 FLATVVLETLKQYTSCHPKTGRKSGKYRKP

FIG. 6

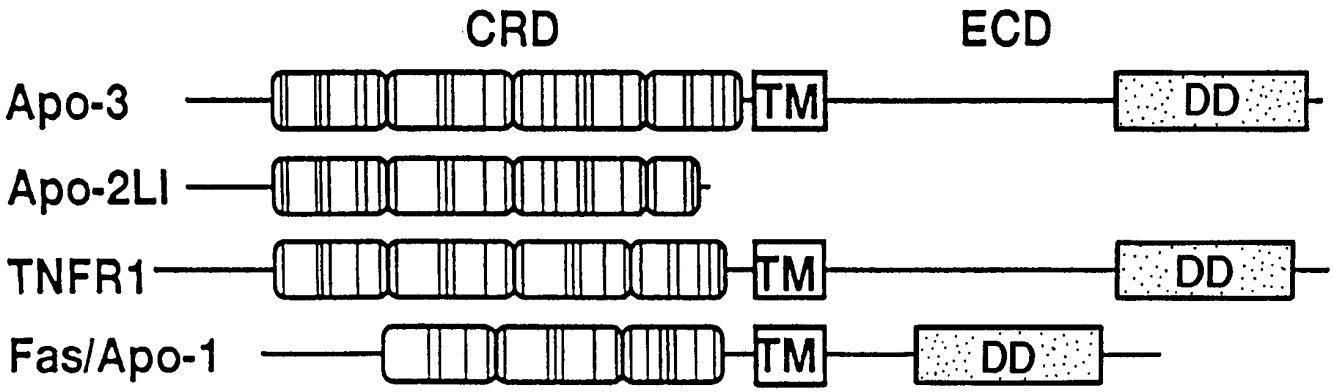

FIG. 7

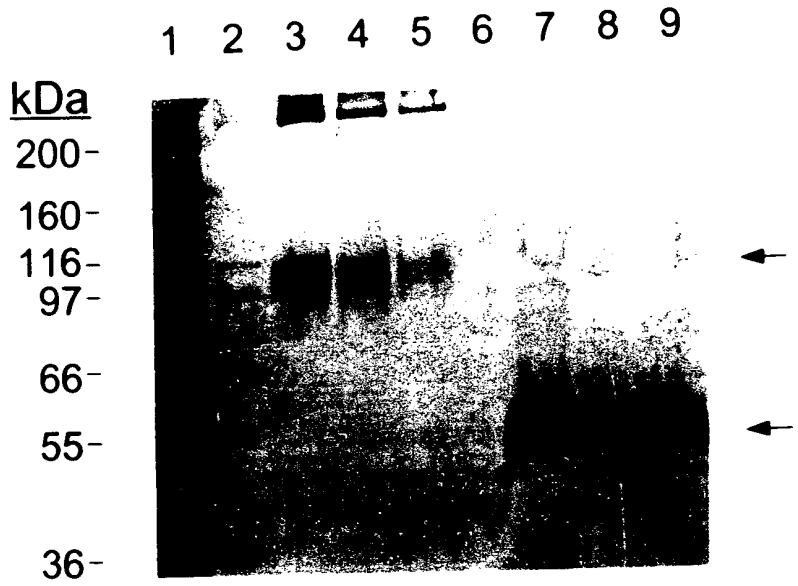

FIG. 3

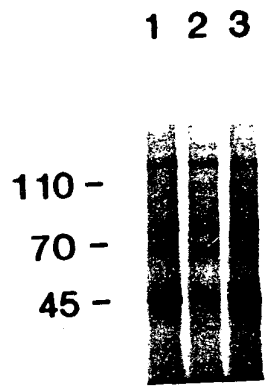

FIG. 8

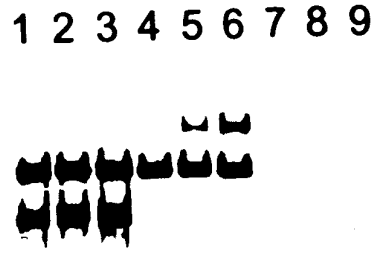

FIG. 10

FIG. 9A

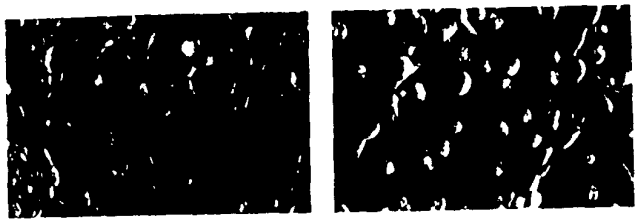

FIG. 9B

FIG. 9C

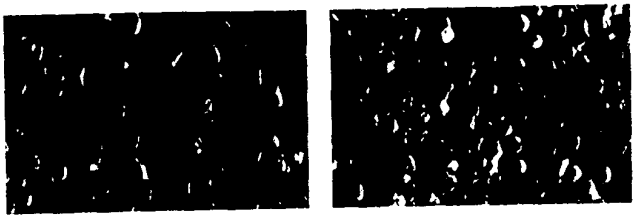

FIG. 9D

FIG. 9E

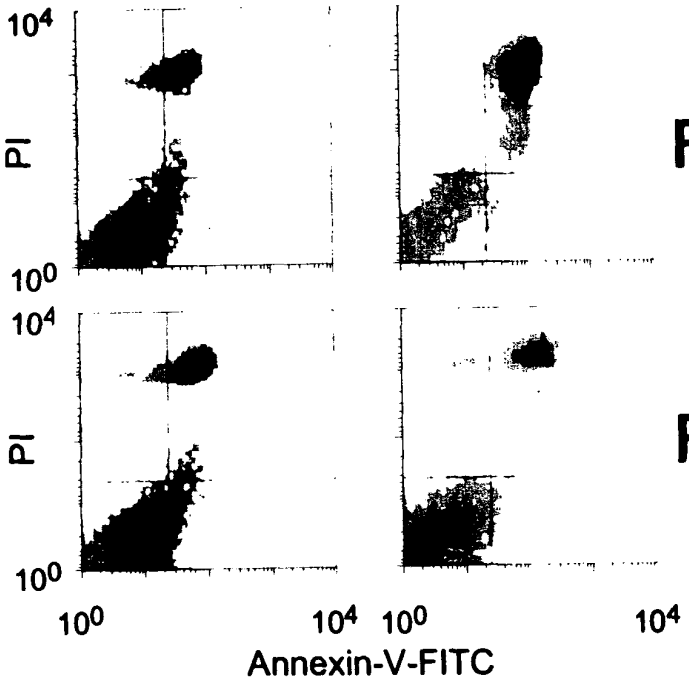

FIG. 9F

FIG. 9G

FIG. 9H

FIG. 9I

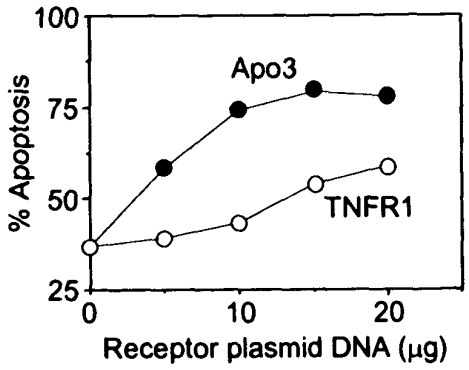

FIG. 9J

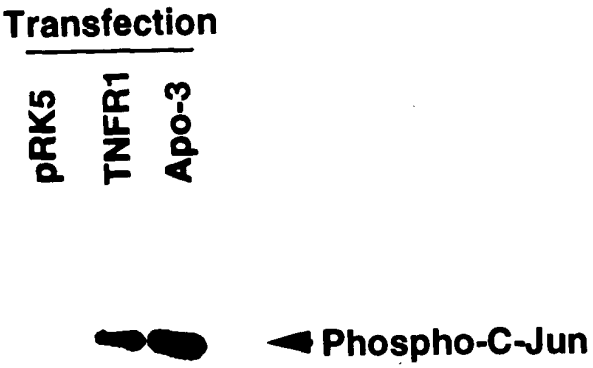
Transfection
pRK5
TNFR1
Apo-3
Phospho-C-Jun

FIG. 11

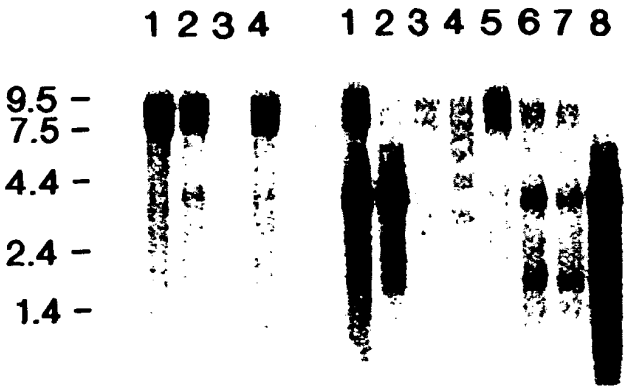
1 2 3 4
1 2 3 4 5 6 7 8
9.5
7.5
4.4
2.4
1.4

FIG. 12